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Proteins containing the forkhead-associated domain (FHA) are known to act in biological processes such as DNA damage repair, protein degradation, and signal transduction. Here we report that DAWDLE (DDL), an FHA domain-containing protein in *Arabidopsis*, acts in the biogenesis of miRNAs and endogenous siRNAs. Unlike mutants of genes known to participate in the processing of miRNA precursors, such as *dcl1*, *hyponastic leaves1*, and *serrate*, *ddl* mutants show reduced levels of pri-miRNAs as well as mature miRNAs. Promoter activity of *MIR* genes, however, is not affected by *ddl* mutations. DDL is an RNA binding protein and is able to interact with DCL1. In addition, we found that SNIP1, the human homolog of DDL, is involved in miRNA biogenesis and interacts with Drosha. Therefore, we uncovered an evolutionarily conserved factor in miRNA biogenesis. We propose that DDL participates in miRNA biogenesis by facilitating DCL1 to access or recognize pri-miRNAs.

DCL1 | microRNA | siRNA | Drosha | SMAD

A class of sequence-specific repressors of gene expression in eukaryotes is 20- to 24-nt small RNAs, which include miRNAs and siRNAs. miRNAs are processed from stem-loop precursor RNAs, called pri-miRNAs. In animals, pri-miRNAs are processed in the nucleus by Drosha to form pre-miRNAs, which are exported to the cytoplasm by exportin 5 and further processed by Dicer to produce mature miRNAs (reviewed in ref. 1). In *Arabidopsis*, mature miRNAs are produced through two processing steps (pri-miRNAs to pre-miRNAs and pre-miRNAs to miRNAs) in the nucleus by DCL1 with the assistance of HYL1 and SERRATE (reviewed in ref. 2). After processing, miRNAs are 2′-O-methylated by HEN1 (3). siRNAs are produced from long, double-stranded RNAs. Plants contain several classes of endogenous siRNAs, such as transacting siRNAs (ta-siRNAs), natural antisense siRNAs (nat-siRNAs), and siRNAs from endogenous repeat sequences and transposons (reviewed in ref. 4).

The forkhead-associated (FHA) domain is an 80- to 100-aa module that is thought to recognize phosphothreonine-containing motifs and mediate protein–protein interactions in prokaryotes and eukaryotes (reviewed in ref. 5). DAWDLE (DDL) is a nuclear-localized FHA domain-containing protein in *Arabidopsis* (6). DDL appears to act in multiple developmental processes such as growth, fertility, and root, shoot, and floral morphogenesis (6).

Smad nuclear interacting protein 1 (SNIP1) is a human FHA domain-containing protein that functions as an inhibitor of TGF-β and NF-κB signaling pathways by competing with the TGF-β signaling protein Smad4 and the NF-κB transcription factor p65/RelA for binding to the transcriptional coactivator p300 (7, 8). Recently, Fujii *et al.* (9) reported that SNIP1 interacts with the transcription factor/oncoprotein c-Myc and enhances its activity by bridging its interaction with p300.

Here we report that DDL is required for the accumulation of miRNAs and endogenous siRNAs in *Arabidopsis*. Its affinity for RNA, its potential association with DCL1, and the reduction in pri-miRNA levels in *ddl* loss-of-function mutants suggest that DDL is a candidate protein recruiting DCL1 to its substrates. In addition, we show that SNIP1 is a human ortholog of DDL and that it also acts in miRNA biogenesis.

Results

DDL Acts in miRNA Biogenesis in *Arabidopsis*. *ddl-1* and *ddl-2* are two recessive, potentially null alleles in the *DDL* gene in the *Wassilewskija* genetic background (6). The *ddl-1* and *ddl-2* mutants show delayed growth and reduced fertility, and have defects in root, shoot, and floral morphology. These pleiotropic developmental defects resemble those of mutants deficient in miRNA biogenesis and prompted us to test whether the *ddl* mutants are compromised in miRNA accumulation. We examined the abundance of various miRNAs in *ddl-1* and *ddl-2* by RNA filter hybridization. Indeed, the levels of 9 of 10 tested DCL1-dependent miRNAs were reduced by 2- to 3.3-fold in *ddl-1* and *ddl-2*, relative to WT [Fig. 1 and supporting information (SI) Fig. S1]. The levels of an antisense miRNA, miR172*, were reduced by 3.3 times in *ddl* mutants (Fig. 1). Introduction of a *DDL* transgene into *ddl-1* rescued the morphological defects of the mutants (6) and fully recovered the levels of miRNAs and miR172* (Fig. 1 and Fig. S1), demonstrating that the defects in miRNA accumulation in the two mutants were due to *DDL* loss of function. To determine whether *DDL* plays a role in the methylation of miRNAs, we evaluated the methylation status of miR161 in *ddl* mutants by treating total RNAs with sodium periodate followed by β-elimination (3) and analyzing miR161 by filter hybridization. Loss of methylation would result in faster migration of the RNA in this assay (3). We found that the *ddl* mutations had no detectable effects on the methylation of miR161 (Fig. S1).

DDL Is Required for the Biogenesis of ta-siRNAs and Repeated DNA-Associated siRNAs. We next tested whether *DDL* is involved in the biogenesis of endogenous siRNAs. We found that two DCL4-dependent siRNAs—siRNA1511, a ta-siRNA from the *TAS2* locus (10), and siRNA255, a ta-siRNA from the *TAS1* locus (10)—were reduced in abundance in *ddl* mutants (Fig. 2*A*). The reduced accumulation of these ta-siRNAs was rescued by the *DDL* trans-

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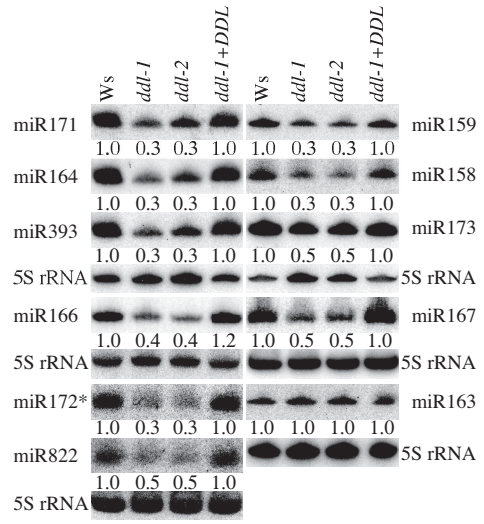

Fig. 1. DDL is required for the accumulation of miRNAs. The accumulation of various miRNAs and miR172* as detected by Northern blotting in Ws (WT), *ddl-1*, *ddl-2*, and a *ddl-1* transgenic line harboring *DDL* genomic DNA. Note that except for miR822, which is DCL4-dependent, all miRNAs are DCL1-dependent. Total RNAs were extracted from inflorescences. The control 5S rRNA blots were below the corresponding miRNA blots. In cases where a membrane was used for several miRNAs, there would be one 5S rRNA blot for several miRNA blots. The numbers indicate the relative abundance of miRNAs or miR172* among the four genotypes.

gene (Fig. 2*A*). Because the ta-siRNAs require a DCL1-dependent miRNA in their biogenesis, the reduction in ta-siRNA accumulation in *ddl* mutants could not support a direct role of DDL in the biogenesis of DCL4-dependent small RNAs. We tested the effect of *ddl* mutations on the accumulation of a DCL4-dependent miRNA, miR822 (11). We found that the *ddl* mutations led to

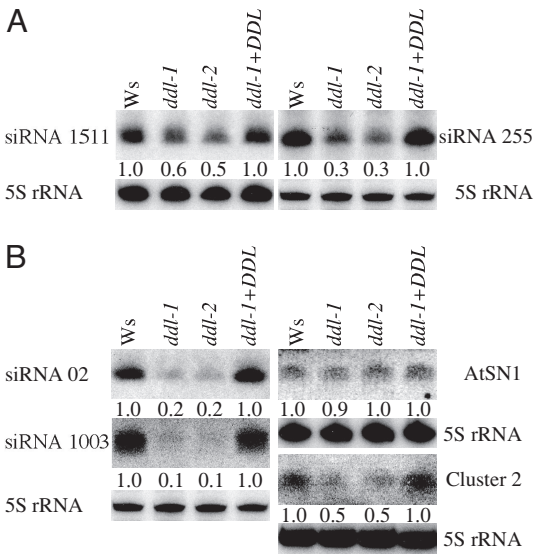

Fig. 2. *DDL* is required for the accumulation of endogenous siRNAs. (*A*) ta-siRNAs were detected in various genotypes by Northern blotting. (*B*) Repeated DNA-associated siRNAs were detected by Northern blotting in various genotypes. The same membrane was used to probe for siRNA 255, siRNA 02, and siRNA 1003, and the corresponding 5S rRNA control is shown twice to aid visual comparison. The numbers below the hybridization images indicate the relative abundance of siRNAs among the four genotypes. Ws, the WT control for the *ddl* mutants; *ddl-1*+*DDL*, a *ddl-1* mutant rescued by *DDL* genomic DNA.

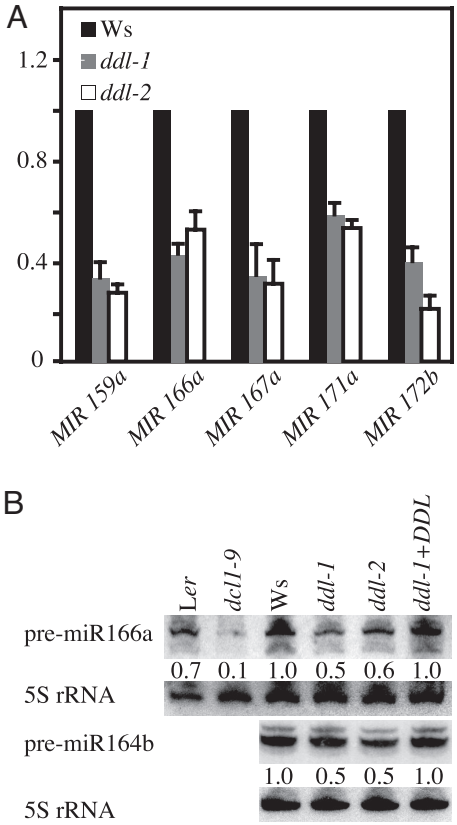

Fig. 3. The accumulation of both pri- and pre-miRNAs in inflorescences is reduced in *ddl* mutants. (*A*) RT-PCR analysis of the levels of pri-miRNAs in WT (Ws), *ddl-1*, and *ddl-2* inflorescences. The levels of pri-miRNAs in *ddl* mutants were normalized to those of *UBIQUITIN 5* and compared with WT. (*B*) Northern blot analysis of pre-miRNAs in various genotypes. L*er*, the WT control for *dcl1-9*; *ddl-1*+*DDL*, a *ddl-1* mutant rescued by *DDL* genomic DNA. The numbers below the hybridization images indicate the relative abundance of pre-miRNAs among the four genotypes.

reduced levels of this miRNA, and that DDL genomic DNA rescued the molecular defect in *ddl-1* (Fig. 1).

We also examined the levels of DCL3-dependent siRNAs from repeated DNA or transposons, such as siRNA02, siRNA1003, AtSN1 siRNAs, and cluster 2 siRNAs. Three of the four siRNAs were reduced by 2- to 10-fold in the *ddl* mutants, and this reduction was rescued by the *DDL* transgene (Fig. 2*B*).

The Amount of pri- and pre-miRNAs Is Reduced in the *ddl* Mutants. To determine the step at which a defect in miRNA biogenesis occurred in *ddl* mutants, we examined the levels of pri-miRNAs and pre-miRNAs in WT and *ddl* mutants. We determined the levels of pri-miRNAs at five *MIR* loci (*MIR159a*, *MIR166a*, *MIR167a*, *MIR171a*, and *MIR172b*) by RT-PCR. The levels of the five tested pri-miRNAs were reduced by 1.7- to 3.0-fold in *ddl-1* and 1.9- to 4.8-fold in *ddl-2* relative to WT (Fig. 3*A*). Next we examined the levels of pre-miR166a and pre-miR164b, which were shown to be detectable by RNA filter hybridization (12). We also included *dcl1-9*, which has reduced levels of pre-miRNAs (12), and its WT control (L*er*) in the analysis. The levels of the two pre-miRNAs were reduced in *ddl* mutants (Fig. 3*B*). Furthermore, in the *ddl* mutants, the levels of pri-miRNAs, pre-miRNAs, and miRNAs appeared to be reduced to a similar extent (Figs. 1 and 3).

DDL Does Not Control the Transcription of *MIR* Genes. The reduction in pri-miRNA levels in *ddl* mutants raised the possibility that DDL is a general transcription factor for *MIR* genes or that DDL is a

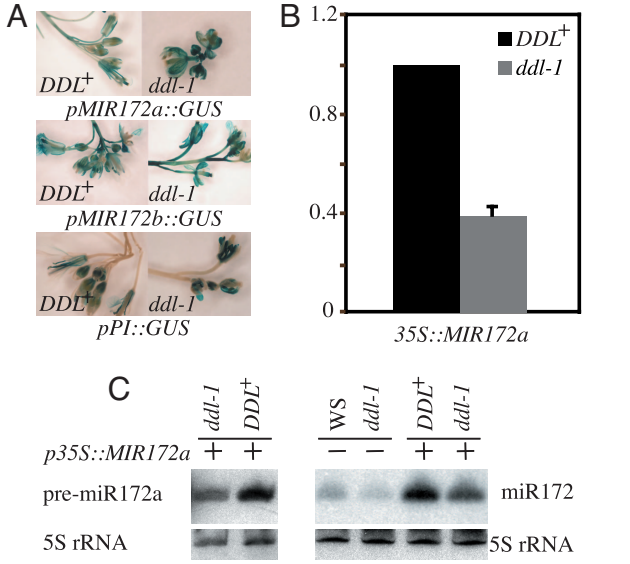

Fig. 4. *DDL* does not act through the promoters of *MIR* genes. (*A*) The *ddl-1* mutation has no obvious effects on GUS expression directed by the promoter of *MIR172a* or *MIR172b*. Many promoter-*GUS* plants were analyzed. A representative image is shown in each case. *DDL*$^+$: *DDL/DDL* or *DDL/ddl-1*. (*B*) RT-PCR analysis of the levels of pri-miR172a in *DDL*$^+$ and *ddl-1* plants harboring a *p35S*::*MIR172a* transgene. (*C*) Northern blotting to determine the accumulation of pre-miR172a and miR172 in *DDL*$^+$ and *ddl-1* plants with (+) or without (−) the *35S*::*MIR172a* transgene.

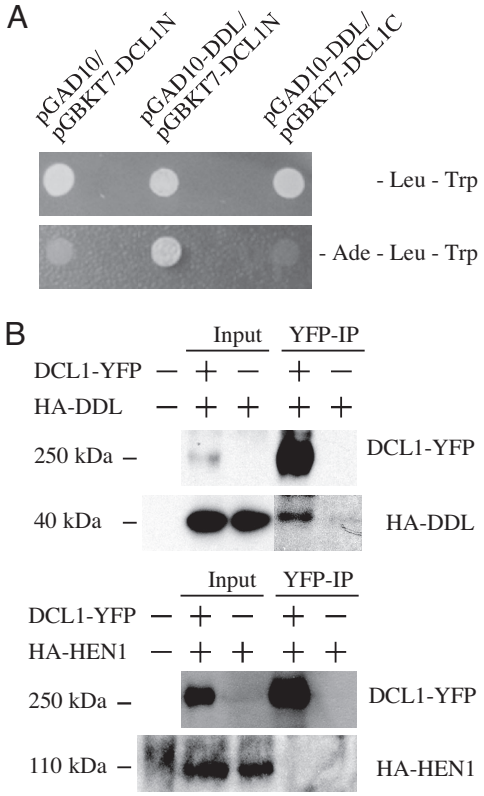

Fig. 5. DDL interacts with DCL1. (*A*) The N-terminal fragment of DCL1 (DCL1N) is necessary and sufficient to interact with DDL in yeast. Interaction between DCL1N with DDL was manifested by the ability of yeast cells (pJ69-4A) to grow in adenine-deficient medium (-Ade–Leu–Trp). The pGBKT7 and pGAD10 vectors contained the DNA binding and activation domains of GAL4, respectively. Yeast colonies containing two plasmids were first selected in -Leu–Trp medium. Then, cells from one colony were resuspended and spotted onto -Leu–Trp–Ade medium. (*B*) CoIP of DDL and DCL1. IP was performed on extracts containing transiently expressed DCL1-YFP and HA-DDL or extracts containing transiently expressed HA-DDL alone by using polyclonal antibodies against GFP and GFP variants. After IP, DCL1-YFP and HA-DDL were detected by using Western blot analysis with anti-GFP and anti-HA antibodies, respectively. CoIP was also performed similarly for DCL1-YFP and HA-HEN1, which served as a control for HA-DDL.

general regulator of transcription for most or all genes. We used two strategies to determine whether *DDL* controls the transcription of *MIR* genes. First, we tested the effect of the *ddl-1* mutation on the expression of a GUS reporter gene under the control of the promoter of *MIR172a* or *MIR172b*. If DDL was a transcriptional regulator of *MIR* genes, the *ddl-1* mutation would be expected to affect the expression of the GUS transgene like it affects the endogenous *MIR* genes. We first generated transgenic lines containing a single-locus *pMIR172a*::*GUS* or *pMIR172b*::*GUS* transgene. The promoters of the two genes were defined as the genomic DNA from the upstream neighboring gene to the start of transcription of *MIR172a* and *MIR172b* as determined by 5′ RACE (data not shown) and were 6.3 kb and 3.4 kb, respectively, for *MIR172a* and *MIR172b*. The transgenic plants were crossed to *ddl-1*, and *DDL*$^+$ (*DDL*/*DDL* or *DDL*/*ddl-1*) or *ddl-1* genotypes containing the GUS transgene were obtained in the F_2 generation. The *ddl-1* mutation did not affect the amount of GUS staining resulting from *pMIR172a*::*GUS* or *pMIR172b*::*GUS* (Fig. 4*A*). Because GUS staining might not be a quantitative measure of transgene expression, we also determined the levels of GUS transcripts from the transgenes by RT-PCR. No difference in GUS transcript levels was found between *DDL*$^+$ and *ddl-1* plants (Fig. S2). In addition, the expression of a GUS reporter driven by the promoter of *PISTILLATA* (13), a protein coding gene, was also similar between *DDL*$^+$ and *ddl* genotypes (Fig. 4*A*), suggesting that *DDL* is unlikely a general regulator of transcription.

Second, we monitored the steady-state levels of pri-miR172a, pre-miR172a, and miR172 in *DDL*$^+$ and *ddl-1* plants containing a single-locus *MIR172a* transgene under the control of the cauliflower mosaic virus 35S promoter. If *DDL* functions as a transcriptional regulator of *MIR172a* through its promoter, the *ddl-1* mutation would not be expected to affect the expression of *MIR172a* driven by the 35S promoter. We crossed a transgenic line containing a single locus of *35S*::*MIR172a* (14) to *ddl-1* and obtained *DDL*$^+$ and *ddl-1* plants containing the transgene in the F_2 generation. As expected, the presence of the *35S*::*MIR172* transgene led to a large increase in the levels of miR172 relative to control Ws plants (Fig. 4*C*; compare lanes with the *35S*::*MIR172a* transgene to those without the transgene), which indicated that the miR172 signal detected in the presence of the transgene largely reflected the miRNA pool produced from the transgene. It was obvious that both miR172 and pre-miR172a levels were reduced in the *ddl-1* mutant (Fig. 4*C*). The levels of pri-miR172a, as determined by RT-PCR, were also reduced in *ddl-1* (Fig. 4*B*). These data demonstrated that DDL did not act through the promoters of *MIR* genes.

DDL Is Associated with DCL1. Because our results did not support a role of *DDL* in the transcriptional control of *MIR* genes, we investigated other possibilities that may explain the reduced levels of miRNAs in *ddl* mutants. One possibility was that *DDL* regulates the expression of genes involved in miRNA biogenesis. We determined the levels of *DCL1*, *HYL1*, and *SERRATE* RNAs by RT-PCR and the levels of HEN1 protein by using Western blot analysis. We found that the *ddl* mutations had no obvious effects on the expression of these genes (data not shown). Next, we tested for interaction of DDL with proteins involved in miRNA biogenesis with a yeast two-hybrid assay and did not detect any interaction between DDL and AGO1, HEN1, or HYL1 (data not shown). However, DDL was found to interact with an N-terminal portion

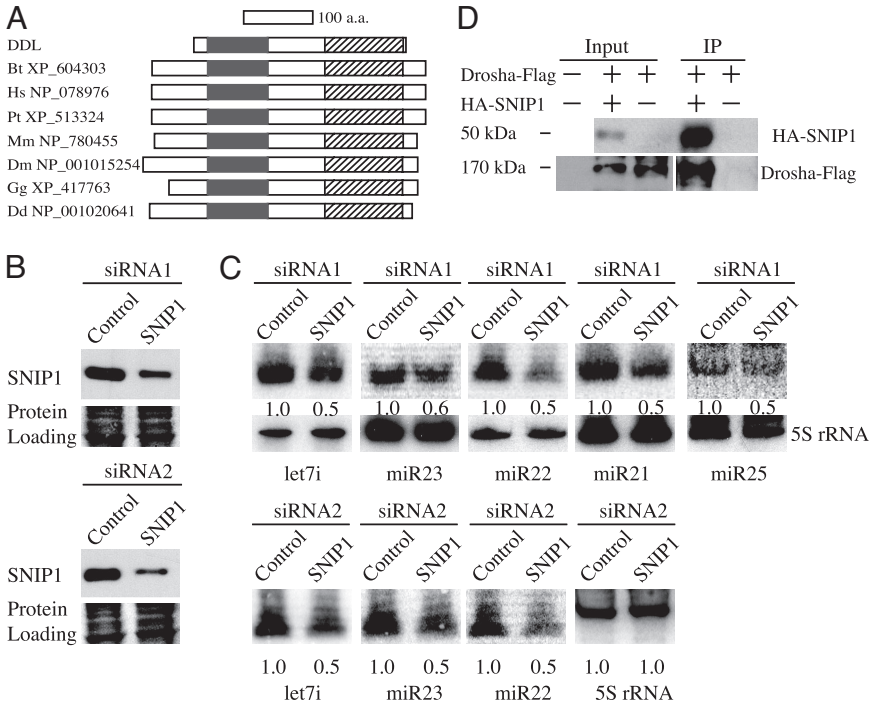

Fig. 6. SNIP1, a human ortholog of DDL, functions in miRNA biogenesis. (*A*) Diagrams show DDL and its homologs in animals. The gray box represents a domain of unknown function (DUF) present in proteins with roles in RNA metabolism. The hatched box indicates the FHA domain. The overall amino acid similarity between DDL and its homologs is 50–60%. The similarity between DDL and its homologs in the DUF and FHA regions is ≈40–50% and 80–90%, respectively. Bt, *Bos taurus*; Hs, *Homo sapiens*; Pt, *Pan troglodytes*; Mm, *Mus musculus*; Dm, *Drosophila melanogaster*; Gg, *Gallus gallus*; Dd, *Danio rerio*. (*B*) The levels of endogenous SNIP1 were reduced in HeLa cells transfected with SNIP1 siRNA1 or siRNA2 as compared with cells transfected with a control nontargeting siRNA. The SNIP protein was detected by using Western blot analysis with anti-SNIP1 antibodies. Part of the stained protein gel is shown below to indicate near equal loading. (*C*) The accumulation of miRNAs as determined by Northern blotting. The signals were quantified with a phosphoimager and normalized against 5S rRNA. The numbers indicate the relative abundance of the miRNAs between control siRNA- and SNIP1 siRNA-treated cells. (*D*) coIP of SNIP1 and Drosha. IP was performed on extracts containing Drosha-Flag and HA-SNIP1 or extracts containing Drosha-Flag alone by using an immobilized anti-HA monoclonal antibody. After IP, Drosha-Flag and HA-SNIP1 were detected by using Western blot analysis with anti-Flag and anti-HA antibodies, respectively. The ''− HA-SNIP1'' lanes represent extracts from cells transfected with the pcDNA3 vector alone. Additional negative controls (Myc-exportin 5 and Dicer) are shown in Fig. S3.

(amino acids 1–833), but not a C-terminal portion (amino acids 814-1909), of DCL1 in the yeast two-hybrid assay (Fig. 5*A*).

To confirm the interaction between DDL and DCL1 with an independent assay, we tested coimmunoprecipitation (coIP) of the two proteins transiently expressed in *Nicotiana benthamiana*. The presence of the viral-silencing suppressor p19 of tomato bushy stunt virus was reported to result in at least a 50-fold increase in the expression of a target protein in a transient expression system in *N. benthamiana* (15). We used this system to separately express the DCL1 protein fused to a yellow fluorescent protein (DCL1-YFP) and the DDL protein fused to an HA epitope (HA-DDL). The HA-DDL extract was then mixed with the DCL1-YFP extract at a 1:1 ratio. We then used anti-GFP (and GFP variants) polyclonal antibodies conjugated to agarose beads to pull down DCL1-YFP from mixed DCL1-YFP/HA-DDL extracts or from HA-DDL extracts alone (control). As shown in Fig. 5*B*, an anti-HA antibody detected the enrichment of HA-DDL in the DCL1-YFP immunoprecipitate relative to the control immunoprecipitate, suggesting the association between DDL and DCL1. As another negative control, we expressed HA-HEN1 and performed coIP on DCL1-YFP and HA-HEN1 with the same procedure. We did not find any association between DCL1-YFP and HA-HEN1 (Fig. 5*B*).

It should be noted that only a small portion of the input HA-DDL was associated with DCL1-YFP in this assay. In fact, HA-DDL was not detected in the DCL1-YFP immunoprecipitate when the levels of DCL1-YFP were low (i.e., in the absence of p19). These observations suggested that only a portion of DCL1 molecules could interact with DDL or that DDL interacted transiently with DCL1.

DDL Is an RNA Binding Protein. BLAST analysis showed that an N-terminal domain of DDL was conserved in several proteins with roles in RNA metabolism (Fig. 6*A*) (data not shown). The presence of this domain prompted us to test whether DDL was an RNA binding protein. We performed a GST pull-down assay to test whether DDL could bind to pri-miR162b, which was transcribed *in vitro* in the presence of [α-^{32}P]UTP. We chose to test pri-miR162b because its 5′ and 3′ ends were determined experimentally (16). GST-DDL or the control GST was expressed in *E. coli* and purified with glutathione beads. Labeled pri-miR162b was added to the beads containing GST-DDL or GST. After washes and elution, the RNA was resolved on a polyacrylamide gel. Pri-miR162b was retained by GST-DDL but not GST alone (Fig. 7 *A* and *B*). Under the same conditions, double-stranded DNA corresponding to pri-miR162b was not retained by GST-DDL (Fig. 7*B*). We found that GST-DDL could also bind to an *in vitro* transcribed RNA corresponding to part of the *APETALA1* mRNA (data not shown). These observations indicate that DDL is an RNA binding protein, but it does not bind specifically to pri-miRNAs *in vitro*.

The Human Homolog of DDL Is Involved in miRNA Biogenesis. By BLAST searches of the nonredundant protein databases of the National Center for Biotechnology Information, we found that the SNIP1 proteins from human, mouse, and other organisms were obvious homologs of DDL (Fig. 6*A*). The human SNIP1 protein was reported to function in TGF-β and NF-κB signaling pathways, but a potential role in miRNA metabolism was not evaluated.

We tested whether the human SNIP1 protein was involved in miRNA biogenesis. We first used an siRNA (siRNA1) targeting SNIP1 to knock down SNIP1 expression in HeLa cells. Indeed, siRNA1 targeting SNIP1 reduced the levels of SNIP1 protein by ≈50% relative to a nontargeting control siRNA (Fig. 6*B*). The accumulation of five tested miRNAs (let-7i, miR21, miR22, miR23, and miR25) showed 1.7- to 2-fold reduction after SNIP1 siRNA1 treatment (Fig. 6*C*). We further tested the effect of a different SNIP1 targeting siRNA (siRNA2). Transfection of HeLa cells with siRNA2 resulted in >50% reduction in SNIP1 protein levels relative to a nontargeting control siRNA (Fig. 6*B*). A 2-fold reduction in three tested miRNAs was observed in siRNA2-treated cells (Fig. 6*C*). These data demonstrated that human SNIP1 functions in miRNA metabolism and is therefore likely an ortholog of DDL.

Both SNIP1 and Drosha, which processes pri-miRNAs in humans, are localized in the nucleus. We reasoned that, like the association between DDL and DCL1, which processes pri-miRNAs in plants, SNIP1 might be associated with Drosha. We tested the

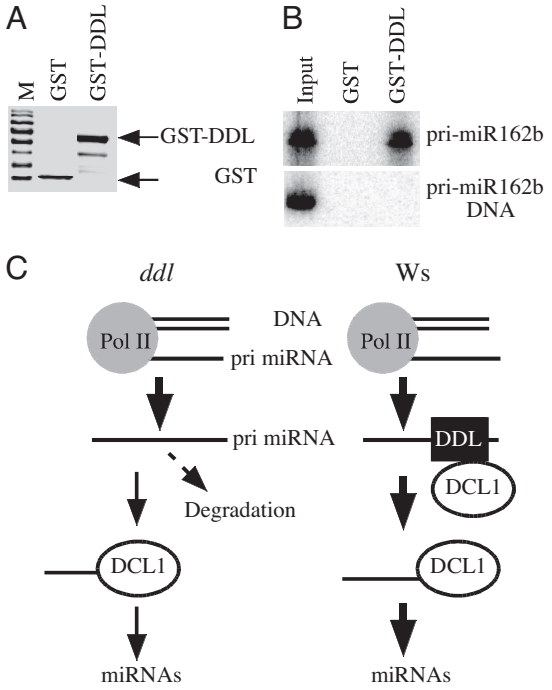

Fig. 7. DDL is an RNA binding protein. (*A*) The two proteins used for the RNA binding assay, GST and GST-DDL, were resolved on an SDS/polyacrylamide gel to show that near equal amounts of the two proteins were used. The lower bands in the GST-DDL lane were truncated GST-DDL proteins because they were all recognized by anti-GST antibodies (data not shown). (*B*) DDL binds pri-miR162b but not DNA *in vitro*. *In vitro*-synthesized and ^{32}P-labeled pri-miR162b or PCR-amplified and labeled DNA corresponding to pri-miR162b was incubated with purified GST or GST-DDL. After washing, the bound nucleic acids were eluted, denatured, and resolved on a polyacrylamide gel. (*C*) A proposed model for DDL's function in miRNA biogenesis. We hypothesize that DDL promotes the access of DCL1 to its substrates. Without DDL, a portion of the pri-miRNA pool cannot be processed by DCL1 and is degraded.

association of SNIP1 and Drosha by coIP. We first transfected 293T cells with an HA-SNIP1 plasmid (8), the vector alone control for HA-SNIP1, or a Drosha-Flag plasmid (17). Western blot analyses showed that HA-SNIP1 and Drosha-Flag were indeed expressed in the transfected cells (Fig. 6*D*, "Input" lanes). Next, we mixed the extract from Drosha-Flag cells with the HA-SNIP1 extract or the vector alone extract and performed coIP. After immunoprecipitation of HA-SNIP1 with an anti-HA antibody, we were able to detect the presence of Drosha-Flag in the SNIP1 immunoprecipitate, but not in the control immunoprecipitate, with an anti-Flag antibody (Fig. 6*D*). To further test the specificity of the SNIP1-Drosha interaction, we performed coIP of SNIP1 and exportin 5 and of SNIP1 and Dicer. We first transfected 293T cells with the HA-SNIP1 plasmid, the vector alone control, a Dicer plasmid (Gregory Hannon, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY), or a Myc-exportin 5 plasmid (18). Next, we confirmed that HA-SNIP1, Dicer, and Myc-exportin 5 were expressed in the cells (Fig. S3, "Input" lanes). We then mixed Myc-exportin 5 or Dicer extracts with the HA-SNIP1 extract or the vector alone extract and performed immunoprecipitation with anti-HA antibodies. Although HA-SNIP1 was successfully immunoprecipitated, neither Dicer nor exportin 5 was detected in the immunoprecipitate (Fig. S3). Therefore, SNIP1 was associated with Drosha *in vivo*.

Discussion

Because miRNAs are crucial regulators of plant development, several genes (*DCL1*, *HYL1*, *HASTY*, *HEN1*, and *SERRATE*) involved in miRNA biogenesis were first identified from forward genetic screens for mutants defective in plant development (19–22). One common feature of these mutants is the pleiotropic developmental defects such as delayed growth, abnormal leaves and flowers, and, in most cases, reduced fertility. In this study, we showed that *DDL*, whose loss-of-function mutations cause pleiotropic developmental defects (6), is also a player in miRNA biogenesis. However, it should be noted that *DDL* must have a broader role than one in miRNA biogenesis because *ddl* mutants have more severe morphological phenotypes than the *dcl1-9* mutant whereas the reduction in miRNA levels is less in *ddl* mutants than in *dcl1-9*.

How does DDL function in miRNA biogenesis? It appears that DDL acts differently from DCL1, SERRATE, and HYL1, which likely form a complex to process pri-miRNAs (23, 24). We found that the amount of pri-miRNAs in *ddl* mutants was reduced, whereas the levels of pri-miRNAs were shown to be increased in *dcl1*, *hyl1*, and *serrate* mutants (12, 25, 26). This argues against a role of DDL in the processing of pri-miRNAs. The reduced accumulation of pri-miRNAs in *ddl* mutants is not due to reduced transcription of *MIR* genes. We hypothesize that DDL promotes the access to, or recognition of, pri-miRNAs by DCL1 (Fig. 7*C*). Without DDL, a portion of pri-miRNAs cannot be properly channeled to DCL1 and is likely degraded, hence the reduced levels of pri-miRNAs in *ddl* mutants. The ability of DDL to interact with DCL1 and the fact that DDL binds RNA are consistent with, but are insufficient to prove, this hypothesis.

DDL not only functions in miRNA biogenesis but also acts in siRNA biogenesis as evidenced by the reduction of ta-siRNAs and repeat-associated siRNAs in *ddl* mutants. Whether DDL is directly involved in ta-siRNA biogenesis is questionable because the biogenesis of ta-siRNAs requires miRNAs that are affected in *ddl* mutants.

However, DDL clearly plays a role in the biogenesis of a DCL4-dependent miRNA and several DCL3-dependent siRNAs. How DDL acts in multiple DCL-dependent processes is currently unknown.

DDL appears to be an evolutionarily conserved protein across plant and animal kingdoms. Because small RNAs are general regulators of gene expression in eukaryotes (reviewed in ref. 1), it is not surprising that some of the machinery involved in the biogenesis or function of small RNAs is present in both plants and animals. Examples include AGO, DICER, HEN1, and exportin 5. DDL can also be added to this list because SNIP1 and DDL show high degrees of sequence similarity, and siRNA-mediated knockdown of SNIP1 results in reduced accumulation of miRNAs in HeLa cells. The association of DDL with DCL1 and the interaction between SNIP1 and Drosha further support a conserved role of DDL and SNIP1 in miRNA biogenesis.

Given that miRNAs in animals regulate large numbers of target genes and play crucial roles in various developmental processes, the fact that SNIP1 acts in miRNA biogenesis would be consistent with the described pleiotropic defects associated with SNIP1 knockdown or overexpression. It was reported that siRNA-mediated knockdown of SNIP1 in human cell lines results in reduced cell proliferation and cell-cycle arrest (27). Knocking down the *C. elegans* SNIP1 protein in a genome-wide RNAi screen results in embryonic lethality (www.wormbase.org). Injection of SNIP1 RNA into dorsal blastomeres of *Xenopus* embryos results in the suppression of dorsal mesoderm fate, which is specified by Nodal (a TGF-β ligand) and the TGF-β signaling pathway (8). Intriguingly, a recent study showed that miR-15 and miR-16 inhibit Nodal/TGF-β signaling by repressing the expression of the Nodal receptor ActRIIA in *Xenopus* (28). One plausible explanation for the inhibitory effect of SNIP1 on dorsal mesoderm fate specification (8) would be that overexpression of SNIP1 leads to increased levels of miR-15 and miR-16, which in turn inhibit Nodal/TGF-β signaling (28).

Although we have uncovered a role of SNIP1 in miRNA biogenesis, SNIP has been found to interact with three transcription

factors as well as with the transcriptional coactivator p300 (7–9). At present, it is not clear whether SNIP1 is a multifunctional protein involved in several molecular processes or whether the observed molecular functions of SNIP1 (interactions with p300 and promotion of miRNA accumulation) represent aspects of a unified function.

Materials and Methods

Plant Materials. The *ddl-1* and *ddl-2* mutants and the *ddl-1* mutant expressing a *DDL* genomic construct were reported by Morris *et al.* (6). To generate *DDL*$^+$ (*DDL/DDL* or *DDL/ddl-1*) or *ddl-1* plants harboring a single-locus GUS transgene, transgenic lines (in L*er* background) containing a single locus of *pMIR172a*::*GUS*, *pMIR172b*::*GUS*, or *pPISTILLATA*::*GUS* (13) were crossed to *ddl-1*. In the F_2 population, plants showing the WT (of the *DDL/DDL* or *DDL/ddl-1* genotypes) and *ddl-1* phenotypes were screened for the GUS transgene by GUS staining. To generate *DDL*$^+$ (*DDL/DDL* or *DDL/ddl-1*) or *ddl-1* plants expressing *35S*::*MIR172a*, we crossed a transgenic line (in L*er* background) containing a single locus of *35S*::*MIR172a* (14) to *ddl-1*. F_2 seeds were selected on Kanamycin medium for the presence of the transgene, and *DDL*$^+$ (*DDL/DDL* or *DDL/ddl-1*) or *ddl-1* plants were identified by their phenotypes.

Plasmid Construction. The construction of GST-DDL, pMIR172a::GUS, and pMIR172b::GUS plasmids is described in *SI Materials and Methods*.

RT-PCR Analysis of pri-miRNAs. cDNA was synthesized from 5 μg of total RNA by using reverse transcriptase (Invitrogen) and oligo(dT). Quantitative PCR was performed in triplicate on a Bio-Rad IQcycler apparatus with the Quantitech SYBR green kit (Bio-Rad). The primers used are listed in Table S1.

RNA Analyses. RNA isolation and hybridization for miRNAs and endogenous siRNAs were performed as described (29). 5′-End-labeled ^{32}P antisense DNA oligonucleotides or LNA oligonucleotides were used to detect miRNAs, ta-siRNAs, AtSN1 siRNA, siRNA02, and siRNA1003. For cluster 2 siRNAs, a DNA fragment was amplified from genomic DNA with forward and reverse primers (Table S1), gel-purified, and labeled by random priming. The detection of pre-miR166a and pre-miR164b was performed as described (12).

GST-DDL RNA binding assays were performed as described (30, 31). A DNA fragment corresponding to pri-miR162b was amplified by PCR from genomic DNA with primers miR162bp1, which contained a T7 promoter, and miR162bp2 (Table S1). The resulting PCR product was purified and used as a template for *in vitro* transcription with T7 polymerase in the presence of [α-^{32}P]UTP to generate pri-miR162b.

Transient Expression in *N. benthamiana* and coIP. Transient expression of DCL1-YFP and HA-DDL was performed as described (32). For coIP between DDL and DCL1, the harvested leaves of *N. benthamiana* were ground in liquid nitrogen and homogenized in 3 vol of protein lysis buffer [50 mM Tris·HCl (pH 8.0), 150 mM NaCl, 0.2% Nonidet P-40, 2 mM DTT, 5% glycerol, complete proteinase inhibitor mixture (Roche)] and centrifuged for 15 min at 16,110 $\times$ *g*. After preclearing with protein-A agarose, half of the HA-DDL or HA-HEN1 lysate was mixed with the DCL1-YFP lysate. The mixed lysate or the HA-DDL or HA-HEN1 lysate alone was incubated with anti-GFP (and GFP variants) antibodies coupled to protein A agarose beads (Clontech) for 2 h. The immune complexes were then washed four times with 1 ml of lysis buffer. Proteins retained on the beads were resolved on SDS/polyacrylamide gels. Anti-YFP (Covance), anti-HA (Sigma-Aldrich), and anti-HEN1 antibodies were used to detect DCL1-YFP, HA-DDL, and HA-HEN1, respectively, by using Western blot analysis.

siRNA-Mediated Knockdown of SNIP1. HeLa cells were transfected with siRNAs targeting SNIP1 or a nontargeting control siRNA (Table S1) (Dharmacon) by using Oligofectamine (Invitrogen). Cells were harvested for protein and RNA analyses 3 days after transfection. Anti-SNIP1 antibodies were purchased from Bethyl Laboratories.

Transient Expression in 293T Cells and CoIP. For details, see *SI Materials and Methods*.

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Supporting Information

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SI Materials and Methods

Plasmid Construction. To generate the GST-DDL plasmid, full-length *DDL* cDNA was amplified from a plasmid with forward and reverse primers (Table S1) and cloned into pGEX-2TK.

The promoter of *MIR172a* was amplified from genomic DNA with primers miR172ap5 and miR172ap6 (Table S1). The promoter of *MIR172b* was amplified from genomic DNA with primers miR172bp1 and miR172bp2 (Table S1). The fragments were cloned into pPZP211-GUS-NOS to generate the promoter-GUS fusion constructs.

Transient Expression in 293T Cells and CoIP. Human 293T cells were transfected with a Drosha-Flag plasmid (pCK-3′flag-Drosha) (1), a human Dicer plasmid (pCDNA3-hDicer), a Myc-exportin 5 plasmid (pKmyc-Exp5) (2), or an HA-SNIP1 plasmid (pCD-5′-HA-c19fulllength) (3) by using Lipofectamine 2000 (Invitrogen). Two days after transfection, cells were harvested and lysed in buffer [50 mM Tris·HCl (pH 8.0), 150 mM NaCl, 0.2% Nonidet P-40, 2 mM DTT, 5% glycerol, complete protease inhibitor mixture (Roche)]. IP was performed by using an immobilized anti-HA monoclonal antibody (Roche). After IP, protein samples were resolved on 8% SDS/polyacrylamide gels. Monoclonal anti-Flag, anti-Myc, and anti-HA antibodies were used to detect Drosha-Flag, Myc-exportin 5, and HA-SNIP1, respectively, by using Western blot analysis.

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2. Yi R, Doehle BP, Qin Y, Macara IG, Cullen BR (2005) Overexpression of exportin 5 enhances RNA interference mediated by short hairpin RNAs and microRNAs. *Rna* 11:220–226.
3. Kim RH, *et al.* (2000) A novel smad nuclear interacting protein, SNIP1, suppresses p300-dependent TGF-beta signal transduction. *Genes Dev* 14:1605–1616.

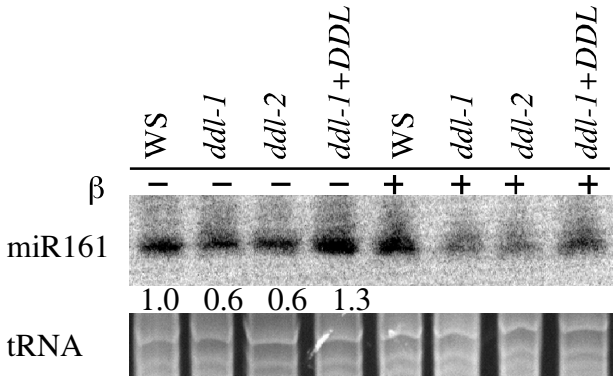

Fig. S1. The methylation of miR161 is not affected by the *ddl* mutations. Total RNAs from Ws (WT), *ddl* mutants, or a *ddl-1* line rescued with *DDL* genomic DNA (*ddl-1* + *DDL*) were either subjected (+) or not subjected (−) to the β elimination reactions (β) and probed for miR161. Because the mobility of miR161 did not change after the β elimination reactions, miR161 was methylated in all four genotypes. The numbers below the hybridization image indicate the relative abundance of miR161 among the four genotypes. A portion of the stained gel is shown below the hybridization image.

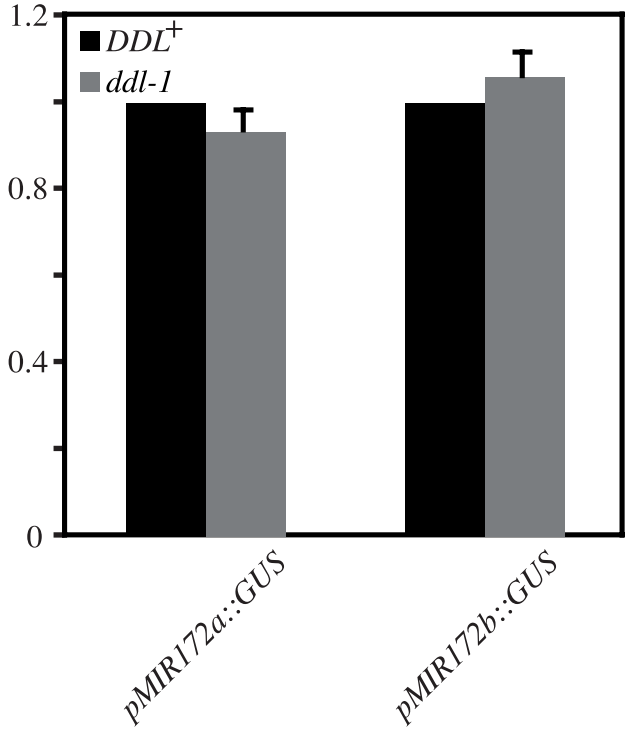

Fig. S2. RT-PCR analysis of the levels of *GUS* mRNA in *DDL*$^+$ and *ddl-1* plants harboring a *pMIR172a*::*GUS* or a *pMIR172b*::*GUS* transgene. The levels of GUS mRNA in the *ddl-1* plants were normalized to those of *UBIQUITIN5* and compared with *DDL*$^+$ plants.

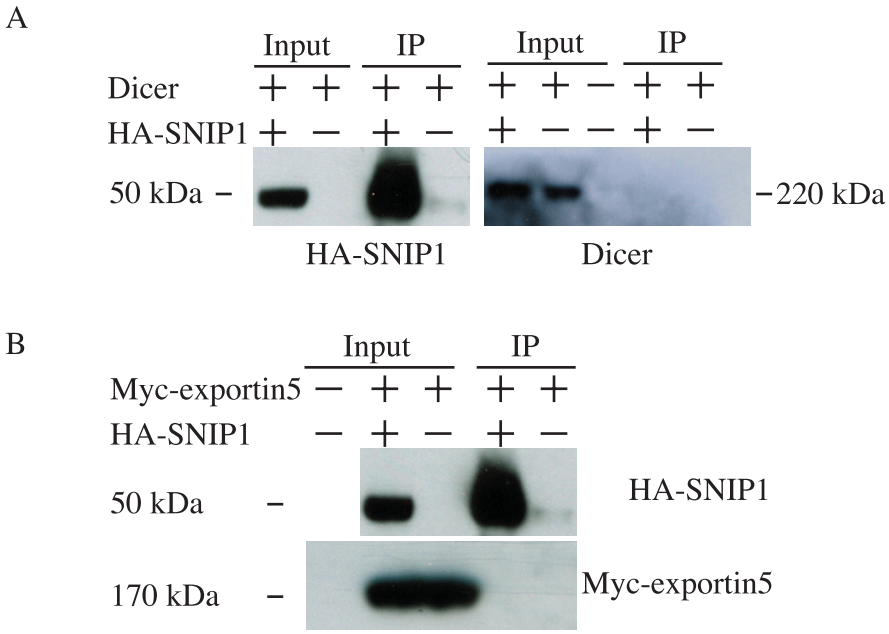

Fig. S3. CoIP of SNIP1 and Dicer or SNIP1 and exportin 5. (*A*) CoIP of SNIP1 and Dicer. Cells (293T) were transfected with a Dicer plasmid, a HA-SNIP1 plasmid, or the vector control for the HA-SNIP1 plasmid (− HA-SNIP1). The extract from cells transfected with the Dicer plasmid was split in two, and the two halves were mixed with the HA-SNIP1 extract or the vector alone extract, respectively. IP was performed by using a monoclonal antibody against HA. After IP, HA-SNIP1 and dicer were detected by using Western blot analysis with anti-HA and anti-Dicer antibodies, respectively. The faint band in the − HA-SNIP1 (IP) lane represents leakage from the neighboring lane. The faint band in the − Dicer (input) lane represents the endogenous Dicer protein in the cells. (*B*) CoIP of exportin 5 and SNIP1. Cells (293 T) were transfected with a Myc-exportin 5 plasmid, a HA-SNIP1 plasmid, or the vector control for the HA-SNIP1 plasmid (− HA-SNIP1). The Myc-exportin 5 extract was split in two, and the two halves were mixed with the HA-SNIP1 extract and the control extract, respectively. IP was performed by using a monoclonal antibody against HA. Following IP, HA-SNIP1 and Myc-exportin 5 were detected by using Western blot analysis with anti-HA and anti-Myc antibodies, respectively. The faint band in the − HA-SNIP1 (IP) lane was due to leakage from the neighboring lane.

Table S1. DNA and RNA oligonucleotides used in this study

Oligonucleotide name	Sequence
	GST-DDL primers
GST-DDL-F	5′-cgcggatccgcgatggctcctagttctaggtctcc-3′
GST-DDL-R	5′-cgcggatccgcgtcactcggcagaattctcgtgc-3′
	MIR172a promoter primers
miR172ap5	5′-taactgcagtagattgggtttagttaaacgagcc-3′
miR172ap6	5′-attctgcagagaaagacctggtgagatctagaa-3′
	MIR172b promoter primers
miR172bp1	5′-gtactgcagcacgagaaaggtacactacaagtgcc-3′
miR172bp2	5′-agactgcagagagaaagggagtgagaggtgcaagtg-3′
	pri-miRNA primers
miR159a-p1	5′-ggagctctacttccatcgtca-3′
miR159a-p2	5′-ccacgttctcatcaaaactttc-3′
miR166a-p1	5′-gactctggctcgctctattca-3′
miR166a-p2	5′-tggtccgaagacgctaaaac-3′
miR167a-p1	5′-gaagctgccagcatgatcta-3′
miR167a-p2	5′-gggtttatagaagggtgcga-3′
miR171a-p1	5′-ccgcgccaatatctcagta-3′
miR171a-p2	5′-tgtctccatttcaacacacaca-3′
miR172a-p1	5′-ccgcgccaatatctcagta-3′
miR172a-p2	5′-aatagtcgttgattgccgatg-3′
miR172b-p1	5′-tctcttgtgcgtgcgtaaat-3′
miR172b-p2	5′-cgcctacaaacaacgacaga-3′
miR162b-p1	5′-taatacgactcactatagggatctatccacctctctctgtaa-3′
miR162b-p2	5′-taacaaacaaacaatttcattttatcc-3′
	UBIQUITIN5 primers
N_UBQ5	5′-ggtgctaagaagaggaagaat-3′
C_UBQ5	5′-ctccttctttctggtaaacgt-3′
	Cluster 2 primers
cluster2-f	5′-ttgctgatttgtattttatgcat-3′
cluster2-r	5′-ctttttcaaaccataaaccagaaa-3′
	SNIP1 siRNAs
siRNA-SNIP1–1S	5′-gaaccgagcccgaggaguuuu-3′
siRNA-SNIP1–1A	5′-aacuccucgggcucgguucuu-3′
siRNA-SNIP1–2S	5′-gcaagucuccucgcagaaguu-3′
siRNA-SNIP1–2A	5′-cuucugcgaggagacuugcuu-3′
siRNA-control-S	5′-uucgcuugcagagagaaucuu-3′
siRNA-control-A	5′-gauucucucugcaagcgaauu-3′